

SEQUENCE LISTING



<110> Werther, George Arthur
Wraight, Christopher John
Edmondson, Stephanie Ruth

<120> METHOD FOR THE PROPHYLAXIS AND/OR
TREATMENT OF MEDICAL DISORDERS

<130> AP32556 071838.0125

<140> 09/598,274

<141> 2000-06-21

<150> 60/140,345

<151> 1999-06-21

<160> 20

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1433

<212> DNA

<213> Human

<220>

<221> polyA_signal

<222> (1416)...(1420)

<221> polyA_site

<222> (1433)...(1433)

<221> CDS

<222> (118)...(1104)

<223> Insulin-like growth factor binding protein
(IGFBP-2)

<221> sig_peptide

<222> (118)...(234)

<221> mat_peptide

<222> (235)...(1101)

<223> mature IGFBP-2

<400> 1

attcggggagc agggaggagg aagaagcgga ggaggcggct cccgctcgca gggccgtgca	60
cctgcccgcc cgcccgctcg ctgctcgcc cgccgcccgc cgctgccgac cgccagc atg	120
Met	

ctg ccg aga gtg ggc tgc ccc gcg ctg ccg ctg ccg ccg ccg ccg ctg Leu Pro Arg Val Gly Cys Pro Ala Leu Pro Leu Pro Pro Pro Pro Leu -35 -30 -25	168
ctg ccg ctg ctg ccg ctg ctg ctg ctg cta ctg ggc gcg agt ggc ggc Leu Pro Leu Leu Pro Leu Leu Leu Leu Leu Gly Ala Ser Gly Gly -20 -15 -10	216
ggc ggc ggg gcg cgc gcg gag gtg ctg ttc cgc tgc ccg ccc tgc aca Gly Gly Gly Ala Arg Ala Glu Val Leu Phe Arg Cys Pro Pro Cys Thr -5 1 5 10	264
ccc gag cgc ctg gcc gcc tgc ggg ccc ccg ccg gtt gcg ccg ccc gcc Pro Glu Arg Leu Ala Ala Cys Gly Pro Pro Val Ala Pro Pro Ala 15 20 25	312
gcg gtg gcc gca gtg gcc gga ggc gcc cgc atg cca tgc gcg gag ctc Ala Val Ala Ala Val Ala Gly Gly Ala Arg Met Pro Cys Ala Glu Leu 30 35 40	360
gtc cgg gag ccg ggc tgc ggc tgc tgc tgc gtg tgc gcc ccg ctg gag Val Arg Glu Pro Gly Cys Gly Cys Cys Ser Val Cys Ala Arg Leu Glu 45 50 55	408
ggc gag gcg tgc ggc gtc tac acc ccg cgc tgc ggc cag ggg ctg cgc Gly Glu Ala Cys Gly Val Tyr Thr Pro Arg Cys Gly Gln Gly Leu Arg 60 65 70	456
tgc tat ccc cac ccg ggc tcc gag ctg ccc ctg cag gcg ctg gtc atg Cys Tyr Pro His Pro Gly Ser Glu Leu Pro Leu Gln Ala Leu Val Met 75 80 85 90	504
ggc gag ggc act tgt gag aag cgc ccg gac gcc gag tat ggc gcc agc Gly Glu Gly Thr Cys Glu Lys Arg Arg Asp Ala Glu Tyr Gly Ala Ser 95 100 105	552
ccg gag cag gtt gca gac aat ggc gat gac cac tca gaa gga ggc ctg Pro Glu Gln Val Ala Asp Asn Gly Asp Asp His Ser Glu Gly Gly Leu 110 115 120	600
gtg gag aac cac gtg gac agc acc atg aac atg ttg ggc ggg gga ggc Val Glu Asn His Val Asp Ser Thr Met Asn Met Leu Gly Gly Gly Gly 125 130 135	648
agt gct ggc ccg aag ccc ctc aag tcg ggt atg aag gag ctg gcc gtg Ser Ala Gly Arg Lys Pro Leu Lys Ser Gly Met Lys Glu Leu Ala Val 140 145 150	696
ttc cgg gag aag gtc act gag cag cac ccg cag atg ggc aag ggt ggc Phe Arg Glu Lys Val Thr Glu Gln His Arg Gln Met Gly Lys Gly Gly 155 160 165 170	744
aag cat cac ctt ggc ctg gag gag ccc aag aag ctg cga cca ccc cct	792

Lys His His Leu Gly Leu Glu Glu Pro Lys Lys Leu Arg Pro Pro Pro	
175 180 185	
gcc agg act ccc tgc caa cag gaa ctg gac cag gtc ctg gag cgg atc	840
Ala Arg Thr Pro Cys Gln Gln Glu Leu Asp Gln Val Leu Glu Arg Ile	
190 195 200	
tcc acc atg cgc ctt ccg gat gag cgg ggc cct ctg gag cac ctc tac	888
Ser Thr Met Arg Leu Pro Asp Glu Arg Gly Pro Leu Glu His Leu Tyr	
205 210 215	
tcc ctg cac atc ccc aac tgt gac aag cat ggc ctg tac aac ctc aaa	936
Ser Leu His Ile Pro Asn Cys Asp Lys His Gly Leu Tyr Asn Leu Lys	
220 225 230	
cag tgc aag atg tct ctg aac ggg cag cgt ggg gag tgc tgg tgt gtg	984
Gln Cys Lys Met Ser Leu Asn Gly Gln Arg Gly Glu Cys Trp Cys Val	
235 240 245 250	
aac ccc aac acc ggg aag ctg atc cag gga gcc ccc acc atc cgg ggg	1032
Asn Pro Asn Thr Gly Lys Leu Ile Gln Gly Ala Pro Thr Ile Arg Gly	
255 260 265	
gac ccc gag tgt cat ctc ttc tac aat gag cag cag gag gct tgc ggg	1080
Asp Pro Glu Cys His Leu Phe Tyr Asn Glu Gln Gln Glu Ala Cys Gly	
270 275 280	
gtg cac acc cag cgg atg cag tag accgcagcca gccggtgcct ggcgcccctg	1134
Val His Thr Gln Arg Met Gln *	
285	
ccccccgccc ctctccaaac accggcagaa aacggagagt gcttgggtgg tgggtgctgg	1194
aggattttcc agttctgaca cacgtattta tatttggaag gagaccagca ccgagctcgg	1254
cacctccccg gcctctctct tcccagctgc agatgccaca cctgctcctt cttgctttcc	1314
ccggggggagg aaggggggttg tggtcgggga gctgggggtac aggtttgggg agggggaaga	1374
gaaattttta tttttgaacc cctgtgtccc ttttgcataa gattaaagga aggaaaagt	1433
<210> 2	
<211> 2474	
<212> DNA	
<213> Human	
<220>	
<221> CDS	
<222> (110)...(985)	
<223> Insulin-like growth factor-binding protein	
(IGFBP-3)	
<400> 2	
ctcagcgccc agccgcttcc tgcctggatt ccacagcttc gcgccgtgta ctgtcgcccc	60
atccctgcgc gccagcctg ccaagcagcg tgccccggtt gcaggcgtc atg cag cgg	118
Met Gln Arg	

gcg cga ccc acg ctc tgg gcc gct gcg ctg act ctg ctg gtg ctg ctc Ala Arg Pro Thr Leu Trp Ala Ala Ala Leu Thr Leu Leu Val Leu Leu 5 10 15	166
cgc ggg ccg ccg gtg gcg cgg gct ggc gcg agc tcg ggg ggc ttg ggt Arg Gly Pro Pro Val Ala Arg Ala Gly Ala Ser Ser Gly Gly Leu Gly 20 25 30 35	214
ccc gtg gtg cgc tgc gag ccg tgc gac gcg cgt gca ctg gcc cag tgc Pro Val Val Arg Cys Glu Pro Cys Asp Ala Arg Ala Leu Ala Gln Cys 40 45 50	262
gcg cct ccg ccc gcc gtg tgc gcg gag ctg gtg cgc gag ccg ggc tgc Ala Pro Pro Pro Ala Val Cys Ala Glu Leu Val Arg Glu Pro Gly Cys 55 60 65	310
ggc tgc tgc ctg acg tgc gca ctg agc gag ggc cag ccg tgc ggc atc Gly Cys Cys Leu Thr Cys Ala Leu Ser Glu Gly Gln Pro Cys Gly Ile 70 75 80	358
tac acc gag cgc tgt ggc tcc ggc ctt cgc tgc cag ccg tcg ccc gac Tyr Thr Glu Arg Cys Gly Ser Gly Leu Arg Cys Gln Pro Ser Pro Asp 85 90 95	406
gag gcg cga ccg ctg cag gcg ctg ctg gac ggc cgc ggg ctc tgc gtc Glu Ala Arg Pro Leu Gln Ala Leu Leu Asp Gly Arg Gly Leu Cys Val 100 105 110 115	454
aac gct agt gcc gtc agc cgc ctg cgc gcc tac ctg ctg cca gcg ccg Asn Ala Ser Ala Val Ser Arg Leu Arg Ala Tyr Leu Leu Pro Ala Pro 120 125 130	502
cca gct cca gga aat gct agt gag tcg gag gaa gac cgc agc gcc ggc Pro Ala Pro Gly Asn Ala Ser Glu Ser Glu Glu Asp Arg Ser Ala Gly 135 140 145	550
agt gtg gag agc ccg tcc gtc tcc agc acg cac cgg gtg tct gat ccc Ser Val Glu Ser Pro Ser Val Ser Ser Thr His Arg Val Ser Asp Pro 150 155 160	598
aag ttc cac ccc ctc cat tca aag ata atc atc atc aag aaa ggg cat Lys Phe His Pro Leu His Ser Lys Ile Ile Ile Ile Lys Lys Gly His 165 170 175	646
gct aaa gac agc cag cgc tac aaa gtt gac tac gag tct cag agc aca Ala Lys Asp Ser Gln Arg Tyr Lys Val Asp Tyr Glu Ser Gln Ser Thr 180 185 190 195	694
gat acc cag aac ttc tcc tcc gag tcc aag cgg gag aca gaa tat ggt Asp Thr Gln Asn Phe Ser Ser Glu Ser Lys Arg Glu Thr Glu Tyr Gly 200 205 210	742

ccc tgc cgt aga gaa atg gaa gac aca ctg aat cac ctg aag ttc ctc	790
Pro Cys Arg Arg Glu Met Glu Asp Thr Leu Asn His Leu Lys Phe Leu	
215 220 225	
aat gtg ctg agt ccc agg ggt gta cac att ccc aac tgt gac aag aag	838
Asn Val Leu Ser Pro Arg Gly Val His Ile Pro Asn Cys Asp Lys Lys	
230 235 240	
gga ttt tat aag aaa aag cag tgt cgc cct tcc aaa ggc agg aag cgg	886
Gly Phe Tyr Lys Lys Lys Gln Cys Arg Pro Ser Lys Gly Arg Lys Arg	
245 250 255	
ggc ttc tgc tgg tgt gtg gat aag tat ggg cag cct ctc cca ggc tac	934
Gly Phe Cys Trp Cys Val Asp Lys Tyr Gly Gln Pro Leu Pro Gly Tyr	
260 265 270 275	
acc acc aag ggg aag gag gac gtg cac tgc tac agc atg cag agc aag	982
Thr Thr Lys Gly Lys Glu Asp Val His Cys Tyr Ser Met Gln Ser Lys	
280 285 290	
tag acgcctgccg caagttaatg tggagctcaa atatgcctta ttttgcacaa	1035
*	

aagactgcc	aggacatgac	cagcagctgg	ctacagcctc	gatttatatt	tctgtttgtg	1095
gtgaactgat	tttttttaa	ccaaagttaa	gaaagagggt	tttgaaatgc	ctatggtttc	1155
tttgaatgg	aaacttgagc	atcttttcac	tttccagtag	tcagcaaaga	gcagtttgaa	1215
ttttcttgtc	gcttcctatc	aaaatattca	gagactcgag	cacagcacc	agacttcatg	1275
cgcccggtga	atgctcacca	catgttggtc	gaagcgccg	accactgact	ttgtgactta	1335
ggcggtgtg	ttgcctatgt	agagaacacg	cttcacccc	actccccgta	cagtgcgcac	1395
aggctttatc	gagaatagga	aaacctttaa	accccggtca	tccggacatc	ccaacgcag	1455
ctcctggagc	tcacagcctt	ctgtggtgtc	atttctgaaa	caagggcggtg	gatecctcaa	1515
ccaagaagaa	tgtttatgtc	ttcaagtgtc	ctgtactgct	tggggactat	tggagaaaat	1575
aaggtggagt	cctacttggt	taaaaaatat	gtatctaaga	atgttctagg	gcactctggg	1635
aacctataaa	ggcaggtatt	tcgggcccctc	ctcttcagga	atcttcctga	agacatggcc	1695
cagtcgaagg	cccaggatgg	cttttgctgc	ggcccggtgg	ggtaggagg	acagagagac	1755
gggagagtca	gcctccacat	tcagaggcat	cacaagtaat	ggcacaattc	ttcggatgac	1815
tgcagaaaat	agtgttttgt	agttcaacaa	ctcaagacga	agcttatttc	tgaggataag	1875
ctcttttaag	gcaaagcttt	attttcatct	ctcatctttt	gtcctcctta	gcacaatgta	1935
aaaaagaata	gtaatatcag	aacaggaagg	aggaatggct	tgctggggag	cccatccagg	1995
acactgggag	cacatagaga	ttcacccatg	tttggtgaac	ttagagtcac	tctcatgctt	2055
ttctttataa	ttcacacata	tatgcagaga	agatatgttc	ttgttaacat	tgtatacaac	2115
atagccccaa	atatagtaag	atctatacta	gataatccta	gatgaaatgt	tagagatgct	2175
atatgataca	actgtggcca	tgactgagga	aaggagctca	cgccagaga	ctgggctgct	2235
ctcccgagg	ccaaacccaa	gaaggtctgg	caaagtcagg	ctcagggaga	ctctgccctg	2295
ctgcagacct	cggtgtggac	acacgctgca	tagagctctc	cttgaaaaca	gaggggtctc	2355
aagacattct	gcctacctat	tagcttttct	ttattttttt	aacttttttg	ggggaaaagt	2415
atttttgaga	agtttgtctt	gcaatgtatt	tataaatagt	aaataaagtt	tttaccatt	2474

<210> 3
 <211> 4989
 <212> DNA
 <213> Human

<220>
<221> sig_peptide
<222> (32)...(121)

<221> mat_peptide
<222> (122)...(4132)

<221> misc_feature
<222> (122)...(2251)
<223> Alpha subunit

<221> misc_feature
<222> (182)...(190)
<223> Potential N-linked glycosylation site

<221> misc_feature
<222> (335)...(343)
<223> Potential N-linked glycosylation site

<221> misc_feature
<222> (434)...(442)
<223> Potential N-linked glycosylation site

<221> misc_feature
<222> (761)...(769)
<223> Potential N-linked glycosylation site

<221> misc_feature
<222> (971)...(979)
<223> Potential N-linked glycosylation site

<221> misc_feature
<222> (1280)...(1288)
<223> Potential N-linked glycosylation site

<221> misc_feature
<222> (1343)...(1351)
<223> Potential N-linked glycosylation site

<221> misc_feature
<222> (1631)...(1639)
<223> Potential N-linked glycosylation site

<221> misc_feature
<222> (1850)...(1858)
<223> Potential N-linked glycosylation site

<221> misc_feature
<222> (1895)...(1903)
<223> Potential N-linked glycosylation site

<221> misc_feature
<222> (1949)...(1957)

<223> Potential N-linked glycosylation site

 <221> misc_feature
 <222> (2240)...(2251)
 <223> Putative proreceptor processing site

 <221> misc_feature
 <222> (2252)...(4132)
 <223> Beta subunit

 <221> misc_feature
 <222> (2270)...(2278)
 <223> Potential N-linked glycosylation site

 <221> misc_feature
 <222> (2297)...(2305)
 <223> Potential N-linked glycosylation site

 <221> misc_feature
 <222> (2321)...(2329)
 <223> Potential N-linked glycosylation site

 <221> misc_feature
 <222> (2729)...(2737)
 <223> Potential N-linked glycosylation site

 <221> misc_feature
 <222> (2768)...(2776)
 <223> Potential N-linked glycosylation site

 <221> misc_feature
 <222> (2837)...(2908)
 <223> Transmembrane region

 <221> misc_feature
 <222> (2918)...(2926)
 <223> Potential N-linked glycosylation site

 <221> misc_binding
 <222> (3047)...(3049)
 <223> Potential ATP binding site

 <221> misc_binding
 <222> (3053)...(3055)
 <223> Potential ATP binding site

 <221> misc_binding
 <222> (3062)...(3064)
 <223> Potential ATP binding site

 <221> misc_binding
 <222> (3128)...(3130)
 <223> Potential ATP binding site

<223> Insulin-like growth factor I receptor (IGF-I receptor)

```

tttttttttt ttttgagaaa gggaatttca t ccc aaa taa aag gaa tga agt      52
Pro Lys  *  Lys Glu  *  Ser
-30

```

ctg	gct	ccg	gag	gag	ggt	ccc	cga	cct	cgc	tgt	ggg	ggc	tcc	tgt	ttc	100
Leu	Ala	Pro	Glu	Glu	Gly	Pro	Arg	Pro	Arg	Cys	Gly	Gly	Ser	Cys	Phe	
-25					-20					-15					-10	

tct ccg ccg cgc tct cgc tct ggc cga cga gtg gag aaa tct gcg ggc 148
Ser Pro Pro Arg Ser Arg Ser Gly Arg Arg Val Glu Lys Ser Ala Gly
-5 1 5

cag gca tcg aca tcc gca acg act atc agc agc tga agc gcc tgg aga 196
Gln Ala Ser Thr Ser Ala Thr Thr Ile Ser Ser * Ser Ala Trp Arg
 10 15 20

act gca cgg tga tgc agg gct acc tcc aca tcc tgc tca tct cca agg 244
Thr Ala Arg * Ser Arg Ala Thr Ser Thr Ser Cys Ser Ser Pro Arg
25 30 35

ccg agg act acc gca gct acc gct tcc cca agc tca cgg tca tta ccg 292
Pro Arg Thr Thr Ala Ala Thr Ala Ser Pro Ser Ser Arg Ser Leu Pro
40 45 50

agt act tgc tgc tgt tcc gag tgg ctg gcc tcg aga gcc tcg gag acc 340
 Ser Thr Cys Cys Cys Ser Glu Trp Leu Ala Ser Arg Ala Ser Glu Thr
 55 60 65

tct tcc cca acc tca cgg tca tcc gcg gct gga aac tct tct aca act 388
Ser Ser Pro Thr Ser Arg Ser Ser Ala Ala Gly Asn Ser Ser Thr Thr
70 75 80 85

acg ccc tgg tca tct tcg aga tga cca atc tca agg ata ttg ggc ttt 436
Thr Pro Trp Ser Ser Ser Arg * Pro Ile Ser Arg Ile Leu Gly Phe
90 95 100

aca acc tga gga aca tta ctc ggg ggg cca tca gga ttg aga aaa atg 484
Thr Thr * Gly Thr Leu Leu Gly Gly Pro Ser Gly Leu Arg Lys Met
105 110 115

ctg	acc	tot	ggt	acc	tct	cca	ctg	tgg	act	ggt	ccc	tga	tcc	tgg	atg	532
Leu	Thr	Ser	Val	Thr	Ser	Pro	Leu	Trp	Thr	Gly	Pro	*	Ser	Trp	Met	
				120					125						130	

cgg tgt cca ata act aca ttg tgg gga ata agc ccc caa agg aat gtg 580
Arg Cys Pro Ile Thr Thr Leu Trp Gly Ile Ser Pro Gln Arg Asn Val
135 140 145

ggg acc tgt gtc cag gga cca tgg agg aga agc cga tgt gtg aga aga Gly Thr Cys Val Gln Gly Pro Trp Arg Arg Ser Arg Cys Val Arg Arg	628
150 155 160	
cca cca tca aca atg agt aca act acc gct gct gga cca caa acc gct Pro Pro Ser Thr Met Ser Thr Thr Thr Ala Ala Gly Pro Gln Thr Ala	676
165 170 175	
gcc aga aaa tgt gcc caa gca cgt gtg gga agc ggg cgt gca ccg aga Ala Arg Lys Cys Ala Gln Ala Arg Val Gly Ser Gly Arg Ala Pro Arg	724
180 185 190	
aca atg agt gct gcc acc ccg agt gcc tgg gca gct gca gcg cgc ctg Thr Met Ser Ala Ala Thr Pro Ser Ala Trp Ala Ala Ala Arg Leu	772
195 200 205 210	
aca acg aca cgg cct gtg tag ctt gcc gcc act act act atg ccg gtg Thr Thr Thr Arg Pro Val * Leu Ala Ala Thr Thr Thr Met Pro Val	820
215 220 225	
tct gtg tgc ctg cct gcc cgc cca aca cct aca ggt ttg agg gct ggc Ser Val Cys Leu Pro Ala Arg Pro Thr Pro Thr Gly Leu Arg Ala Gly	868
230 235 240	
gct gtg tgg acc gtg act tct gcg cca aca tcc tca gcg ccg aga gca Ala Val Trp Thr Val Thr Ser Ala Pro Thr Ser Ser Ala Pro Arg Ala	916
245 250 255	
gcg act ccg agg ggt ttg tga tcc acg acg gcg agt gca tgc agg agt Ala Thr Pro Arg Gly Leu * Ser Thr Thr Ala Ser Ala Cys Arg Ser	964
260 265 270	
gcc cct cgg gct tca tcc gca acg gca gcc aga gca tgt act gca tcc Ala Pro Arg Ala Ser Ser Ala Thr Ala Ala Arg Ala Cys Thr Ala Ser	1012
275 280 285	
ctt gtg aag gtc ctt gcc cga agg tct gtg agg aag aaa aga aaa caa Leu Val Lys Val Leu Ala Arg Arg Ser Val Arg Lys Lys Arg Lys Gln	1060
290 295 300	
aga cca ttg att ctg tta ctt ctg ctc aga tgc tcc aag gat gca cca Arg Pro Leu Ile Leu Leu Leu Leu Arg Cys Ser Lys Asp Ala Pro	1108
305 310 315 320	
tct tca agg gca att tgc tca tta aca tcc gac ggg gga ata aca ttg Ser Ser Arg Ala Ile Cys Ser Leu Thr Ser Asp Gly Gly Ile Thr Leu	1156
325 330 335	
ctt cag agc tgg aga act tca tgg ggc tca tcg agg tgg tga cgg gct Leu Gln Ser Trp Arg Thr Ser Trp Gly Ser Ser Arg Trp * Arg Ala	1204
340 345 350	

acg tga aga tcc gcc att ctc atg cct tgg tct cct tgt cct tcc taa	1252
Thr * Arg Ser Ala Ile Leu Met Pro Trp Ser Pro Cys Pro Ser *	
355 360 365	
aaa acc ttc gcc tca tcc tag gag agg agc agc tag aag gga att act	1300
Lys Thr Phe Ala Ser Ser * Glu Arg Ser Ser * Lys Gly Ile Thr	
370 375	
cct tct acg tcc tcg aca acc aga act tgc agc aac tgt ggg act ggg	1348
Pro Ser Thr Ser Ser Thr Thr Arg Thr Cys Ser Asn Cys Gly Thr Gly	
380 385 390 395	
acc acc gca acc tga cca tca aag cag gga aaa tgt act ttg ctt tca	1396
Thr Thr Ala Thr * Pro Ser Lys Gln Gly Lys Cys Thr Leu Leu Ser	
400 405 410	
atc cca aat tat gtg ttt ccg aaa ttt acc gca tgg agg aag tga cgg	1444
Ile Pro Asn Tyr Val Phe Pro Lys Phe Thr Ala Trp Arg Lys * Arg	
415 420 425	
gga cta aag ggc gcc aaa gca aag ggg aca taa aca cca gga aca acg	1492
Gly Leu Lys Gly Ala Lys Ala Lys Gly Thr * Thr Pro Gly Thr Thr	
430 435 440	
ggg aga gag cct cct gtg aaa gtg acg tcc tgc att tca cct cca cca	1540
Gly Arg Glu Pro Pro Val Lys Val Thr Ser Cys Ile Ser Pro Pro Pro	
445 450 455	
cca cgt cga aga atc gca tca tca taa cct ggc acc ggt acc ggc ccc	1588
Pro Arg Arg Arg Ile Ala Ser Ser * Pro Gly Thr Gly Thr Gly Pro	
460 465 470	
ctg act aca ggg atc tca tca gct tca ccg ttt act aca agg aag cac	1636
Leu Thr Thr Gly Ile Ser Ser Ala Ser Pro Phe Thr Thr Arg Lys His	
475 480 485	
cct tta aga atg tca cag agt atg atg ggc agg atg cct gcg gct cca	1684
Pro Leu Arg Met Ser Gln Ser Met Met Gly Arg Met Pro Ala Ala Pro	
490 495 500	
aca gct gga aca tgg tgg acg tgg acc tcc cgc cca aca agg acg tgg	1732
Thr Ala Gly Thr Trp Trp Thr Trp Thr Ser Arg Pro Thr Arg Thr Trp	
505 510 515	
agc ccg gca tct tac tac atg ggc tga agc cct gga ctc agt acg ccg	1780
Ser Pro Ala Ser Tyr Tyr Met Gly * Ser Pro Gly Leu Ser Thr Pro	
520 525 530	
ttt acg tca agg ctg tga ccc tca cca tgg tgg aga acg acc ata tcc	1828
Phe Thr Ser Arg Leu * Pro Ser Pro Trp Trp Arg Thr Thr Ile Ser	
535 540 545	
gtg ggg cca aga gtg aga tct tgt aca ttc gca cca atg ctt cag ttc	1876

Val Gly Pro Arg Val Arg Ser Cys Thr Phe Ala Pro Met Leu Gln Phe	
550 555 560 565	
ctt cca ttc cct tgg acg ttc ttt cag cat cga act cct ctt ctc agt	1924
Leu Pro Phe Pro Trp Thr Phe Phe Gln His Arg Thr Pro Leu Leu Ser	
570 575 580	
taa tcg tga agt gga acc ctg cct ctc tgc cca acg gca acc tga gtt	1972
* Ser * Ser Gly Thr Leu Pro Leu Cys Pro Thr Ala Thr * Val	
585 590	
act aca ttg tgc gct ggc agc ggc agc ctc agg acg gct acc ttt acc	2020
Thr Thr Leu Cys Ala Gly Ser Gly Ser Leu Arg Thr Ala Thr Phe Thr	
595 600 605 610	
ggc aca att act gct cca aag aca aaa tcc cca tca gga agt atg ccg	2068
Gly Thr Ile Thr Ala Pro Lys Thr Lys Ser Pro Ser Gly Ser Met Pro	
615 620 625	
acg gca cca tcg aca ttg agg agg tca cag aga acc cca aga ctg agg	2116
Thr Ala Pro Ser Thr Leu Arg Arg Ser Gln Arg Thr Pro Arg Leu Arg	
630 635 640	
tgt gtg gtg ggg aga aag ggc ctt gct gcg cct gcc cca aaa ctg aag	2164
Cys Val Val Gly Arg Lys Gly Leu Ala Ala Pro Ala Pro Lys Leu Lys	
645 650 655	
ccg aga agc agg ccg aga agg agg agg ctg aat acc gca aag tct ttg	2212
Pro Arg Ser Arg Pro Arg Arg Arg Leu Asn Thr Ala Lys Ser Leu	
660 665 670	
aga att tcc tgc aca act cca tct tcg tgc cca gac ctg aaa gga agc	2260
Arg Ile Ser Cys Thr Thr Pro Ser Ser Cys Pro Asp Leu Lys Gly Ser	
675 680 685 690	
gga gag atg tca tgc aag tgg cca aca cca cca tgt cca gcc gaa gca	2308
Gly Glu Met Ser Cys Lys Trp Pro Thr Pro Pro Cys Pro Ala Glu Ala	
695 700 705	
gga aca cca cgg ccg cag aca cct aca aca tca ccg acc cgg aag agc	2356
Gly Thr Pro Arg Pro Gln Thr Pro Thr Thr Ser Pro Thr Arg Lys Ser	
710 715 720	
tgg aga cag agt acc ctt tct ttg aga gca gag tgg ata aca agg aga	2404
Trp Arg Gln Ser Thr Leu Ser Leu Arg Ala Glu Trp Ile Thr Arg Arg	
725 730 735	
gaa ctg tca ttt cta acc ttc ggc ctt tca cat tgt acc gca tcg ata	2452
Glu Leu Ser Phe Leu Thr Phe Gly Leu Ser His Cys Thr Ala Ser Ile	
740 745 750	
tcc aca gct gca acc acg agg ctg aga agc tgg gct gca gcg cct cca	2500
Ser Thr Ala Ala Thr Thr Arg Leu Arg Ser Trp Ala Ala Ala Pro Pro	

755	760	765	770	
act tcg tct ttg caa gga cta tgc ccg cag aag gag cag atg aca ttc				2548
Thr Ser Ser Leu Gln Gly Leu Cys Pro Gln Lys Glu Gln Met Thr Phe				
775		780	785	
ctg ggc cag tga cct ggg agc caa ggc ctg aaa act cca tct ttt taa				2596
Leu Gly Gln * Pro Gly Ser Gln Gly Leu Lys Thr Pro Ser Phe *				
790		795	800	
agt ggc cgg aac ctg aga atc cca atg gat tga ttc taa tgt atg aaa				2644
Ser Gly Arg Asn Leu Arg Ile Pro Met Asp * Phe * Cys Met Lys				
805		810		
taa aat acg gat cac aag ttg agg atc agc gag aat gtg tgt cca gac				2692
* Asn Thr Asp His Lys Leu Arg Ile Ser Glu Asn Val Cys Pro Asp				
815		820	825	
agg aat aca gga agt atg gag ggg cca agc taa acc ggc taa acc cgg				2740
Arg Asn Thr Gly Ser Met Glu Gly Pro Ser * Thr Gly * Thr Arg				
830		835	840	
gga act aca cag ccc gga ttc agg cca cat ctc tct ctg gga atg ggt				2788
Gly Thr Thr Gln Pro Gly Phe Arg Pro His Leu Ser Leu Gly Met Gly				
845		850	855	
cgt gga cag atc ctg tgt tct tct atg tcc agg cca aaa cag gat atg				2836
Arg Gly Gln Ile Leu Cys Ser Ser Met Ser Arg Pro Lys Gln Asp Met				
860		865	870	875
aaa act tca tcc atc tga tca tcg ctc tgc ccg tcg ctg tcc tgt tga				2884
Lys Thr Ser Ser Ile * Ser Ser Leu Cys Pro Ser Leu Ser Cys *				
880		885		
tcg tgg gag ggt tgg tga tta tgc tgt acg tct tcc ata gaa aga gaa				2932
Ser Trp Glu Gly Trp * Leu Cys Cys Thr Ser Ser Ile Glu Arg Glu				
890		895	900	
ata aca gca ggc tgg gga atg gag tgc tgt atg cct ctg tga acc cgg				2980
Ile Thr Ala Gly Trp Gly Met Glu Cys Cys Met Pro Leu * Thr Arg				
905		910	915	
agt act tca gcg ctg ctg atg tgt acg ttc ctg atg agt ggg agg tgg				3028
Ser Thr Ser Ala Leu Leu Met Cys Thr Phe Leu Met Ser Gly Arg Trp				
920		925	930	935
ctc ggg aga aga tca cca tga gcc ggg aac ttg ggc agg ggt cgt ttg				3076
Leu Gly Arg Arg Ser Pro * Ala Gly Asn Leu Gly Arg Gly Arg Leu				
940		945	950	
gga tgg tct atg aag gag ttg cca agg gtg tgg tga aag atg aac ctg				3124
Gly Trp Ser Met Lys Glu Leu Pro Arg Val Trp * Lys Met Asn Leu				
955		960	965	

aaa cca gag tgg cca tta aaa cag tga acg agg ccg caa gca tgc gtg	3172
Lys Pro Glu Trp Pro Leu Lys Gln * Thr Arg Pro Gln Ala Cys Val	
970 975 980	
aga gga ttg agt ttc tca acg aag ctt ctg tga tga agg agt tca att	3220
Arg Gly Leu Ser Phe Ser Thr Lys Leu Leu * * Arg Ser Ser Ile	
985 990	
gtc acc atg tgg tgc gat tgc tgg gtg tgg tgt ccc aag gcc agc caa	3268
Val Thr Met Trp Cys Asp Cys Trp Val Trp Cys Pro Lys Ala Ser Gln	
995 1000 1005 1010	
cac tgg tca tca tgg aac tga tga cac ggg gcg atc tca aaa gtt atc	3316
His Trp Ser Ser Trp Asn * * His Gly Ala Ile Ser Lys Val Ile	
1015 1020	
tcc ggt ctc tga ggc cag aaa tgg aga ata atc cag tcc tag cac ctc	3364
Ser Gly Leu * Gly Gln Lys Trp Arg Ile Ile Gln Ser * His Leu	
1025 1030 1035	
caa gcc tga gca aga tga ttc aga tgg ccg gag aga ttg cag acg gca	3412
Gln Ala * Ala Arg * Phe Arg Trp Pro Glu Arg Leu Gln Thr Ala	
1040 1045 1050	
tgg cat acc tca acg cca ata agt tcg tcc aca gag acc ttg ctg ccc	3460
Trp His Thr Ser Thr Pro Ile Ser Ser Ser Thr Glu Thr Leu Leu Pro	
1055 1060 1065	
gga att gca tgg tag ccg aag att tca cag tca aaa tcg gag att ttg	3508
Gly Ile Ala Trp * Pro Lys Ile Ser Gln Ser Lys Ser Glu Ile Leu	
1070 1075 1080	
gta tga cgc gag ata tct atg aga cag act att acc gga aag gag gca	3556
Val * Arg Glu Ile Ser Met Arg Gln Thr Ile Thr Gly Lys Glu Ala	
1085 1090 1095	
aag ggc tgc tgc ccg tgc gct gga tgt ctc ctg agt ccc tca agg atg	3604
Lys Gly Cys Cys Pro Cys Ala Gly Cys Leu Leu Ser Pro Ser Arg Met	
1100 1105 1110	
gag tct tca cca ctt act cgg acg tct ggt cct tcg ggg tcg tcc tct	3652
Glu Ser Ser Pro Leu Thr Arg Thr Ser Gly Pro Ser Gly Ser Ser Ser	
1115 1120 1125 1130	
ggg aga tcg cca cac tgg ccg agc agc cct acc agg gct tgt cca acg	3700
Gly Arg Ser Pro His Trp Pro Ser Ser Pro Thr Arg Ala Cys Pro Thr	
1135 1140 1145	
agc aag tcc ttc gct tcg tca tgg agg gcg gcc ttc tgg aca agc cag	3748
Ser Lys Ser Phe Ala Ser Ser Trp Arg Ala Ala Phe Trp Thr Ser Gln	
1150 1155 1160	

aca act gtc ctg aca tgc tgt ttg aac tga tgc gca tgt gct ggc agt Thr Thr Val Leu Thr Cys Cys Leu Asn * Cys Ala Cys Ala Gly Ser 1165 1170 1175	3796
ata acc cca aga tga ggc ctt cct tcc tgg aga tca tca gca gca tca Ile Thr Pro Arg * Gly Leu Pro Ser Trp Arg Ser Ser Ala Ala Ser 1180 1185 1190	3844
aag agg aga tgg agc ctg gct tcc ggg agg tct cct tct act aca gcg Lys Arg Arg Trp Ser Leu Ala Ser Gly Arg Ser Pro Ser Thr Thr Ala 1195 1200 1205	3892
agg aga aca agc tgc ccg agc ccg agg agc tgg acc tgg agc cag aga Arg Arg Thr Ser Cys Pro Ser Arg Arg Ser Trp Thr Trp Ser Gln Arg 1210 1215 1220	3940
aca tgg aga gcg tcc ccc tgg acc cct ccg cct cct cgt cct ccc tgc Thr Trp Arg Ala Ser Pro Trp Thr Pro Arg Pro Pro Arg Pro Pro Cys 1225 1230 1235 1240	3988
cac tgc ccg aca gac act cag gac aca agg ccg aga acg gcc ccg gcc His Cys Pro Thr Asp Thr Gln Asp Thr Arg Pro Arg Thr Ala Pro Ala 1245 1250 1255	4036
ctg ggg tgc tgg tcc tcc gcg cca gct tgc acg aga gac agc ctt acg Leu Gly Cys Trp Ser Ser Ala Pro Ala Ser Thr Arg Asp Ser Leu Thr 1260 1265 1270	4084
ccc aca tga acg ggg gcc gca aga acg agc ggg cct tgc cgc tgc ccc Pro Thr * Thr Gly Ala Ala Arg Thr Ser Gly Pro Cys Arg Cys Pro 1275 1280 1285	4132
agtcttcgac ctgctgatcc ttggatcctg aatctgtgca aacagtaacg tgtgcgcacg cgcagcgggg tgggggggga gagagagttt taacaatcca ttcacaagcc tcctgtacct cagtggatct tcagttctgc ccttgcctgc ccgaggagac agcttctctg cagtaaaaca catttgggat gttccttttt tcaatatgca agcagctttt tattccctgc ccaaaccctt aactgacatg ggcctttaag aaccttaatg acaacactta atagcaacag agcacttgag aaccagtctc ctcactctgt cctgtcctt cctgtttctc cctttctctc tcctctctgc ttcataacgg aaaaataatt gccacaagtc cagctgggaa gcccttttta tcagtttgag gaagtggctg tccctgtggc cccatccaac cactgtacac accgcctga caccgtgggt cattacaaaa aaacacgtgg agatggaaat ttttaccttt atctttcacc tttctagggg catgaaattt acaaagggcc atcgttcatc caaggctgtt accattttaa cgctgcctaa ttttgccaaa atcctgaact ttctccctca tcggcccggc gctgattcct cgtgtccgga ggcatgggtg agcatggcag ctggttgctc catttgagag acacgctggc gacacactcc gtccatccga ctgcccctgc tgtgctgctc aaggccacag gcacacaggt ctcattgctt ctgactagat tattatttgg gggaactgga cacaataggt ctttctctca gtgaagggtg ggagaagctg aaccggc	4192 4252 4312 4372 4432 4492 4552 4612 4672 4732 4792 4852 4912 4972 4989

<210> 4
 <211> 25
 <212> DNA
 <213> Human

<400> 4	
gcgcccgcgtg catgacgcct gcaac	25
<210> 5	
<211> 24	
<212> DNA	
<213> Human	
<400> 5	
cgggcggctc acctggagct ggcg	24
<210> 6	
<211> 18	
<212> DNA	
<213> Human	
<400> 6	
aggcggctga cggcacta	18
<210> 7	
<211> 19	
<212> DNA	
<213> Human	
<400> 7	
caggcgtcat gcagcgggc	19
<210> 8	
<211> 25	
<212> DNA	
<213> Human	
<400> 8	
cggagatgcc gcatgccagc gcagg	25
<210> 9	
<211> 18	
<212> DNA	
<213> Human	
<400> 9	
gacagcgtcg gagcgatc	18
<210> 10	
<211> 18	
<212> DNA	
<213> Human	
<400> 10	
atctctccgc ttcctttc	18
<210> 11	
<211> 18	

<212> DNA	
<213> Human	
<400> 11	
gaaaggaagc ggagagat	18
<210> 12	
<211> 15	
<212> RNA	
<213> Human	
<400> 12	
uccggagcca gacuu	15
<210> 13	
<211> 15	
<212> RNA	
<213> Human	
<400> 13	
cacaguugcu gcaag	15
<210> 14	
<211> 15	
<212> RNA	
<213> Human	
<400> 14	
ucuccgcuuc cuuuc	15
<210> 15	
<211> 15	
<212> RNA	
<213> Human	
<400> 15	
agccccaca gcgag	15
<210> 16	
<211> 15	
<212> RNA	
<213> Human	
<400> 16	
gccuuggaga ugagc	15
<210> 17	
<211> 15	
<212> RNA	
<213> Human	
<400> 17	
uaacagaggu cagca	15

<210> 18
<211> 15
<212> RNA
<213> Human

<400> 18
ggaucagggg- ccagu 15

<210> 19
<211> 15
<212> RNA
<213> Human

<400> 19
cggcaagcua cacag 15

<210> 20
<211> 15
<212> RNA
<213> Human

<400> 20
ggcaggcagg cacac 15